

Be #5

PCT09

RAW SEQUENCE LISTING

DATE: 06/26/2001

PATENT APPLICATION: US/09/763,909

TIME: 08:56:43

Input Set : A:\13005 002001.TXT

Output Set: N:\CRF3\06262001\I763909.raw

ENTERED

4 <110> APPLICANT: Dikstein, Rivka
5 Yamit-Hezi, Ayala
7 <120> TITLE OF INVENTION: A TRANSCRIPTION FACTOR TFIID SUBUNIT,
8 TAFII105, POLYPEPTIDES, DNA ENCODING THEREFOR AND
9 PHARMACEUTICAL COMPOSITIONS
12 <130> FILE REFERENCE: 13005/002001
14 <140> CURRENT APPLICATION NUMBER: 09/763,909
15 <141> CURRENT FILING DATE: 2001-02-26
17 <160> NUMBER OF SEQ ID NOS: 6
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2558
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
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28 aggctgcctg ctctcagat agtcgccgtg aaagccccc acaccacgac aatccagttt 120
29 cctgctaatt tgcagcttcc tccaggaacc gttttgatta aaagtaacag tggtcgcgtg 180
30 atgttggtat ctctcagca aactgtaaca agagccgaga ccacaagtaa cataacctca 240
31 aggccagcag taccagegaa tctcaaaca gtcaaatct gtacagtgcc gaactctagc 300
32 tcacaattaa tcaagaaagt ggcagtgaca cctgttaaaa aattggcaca aataggaact 360
33 actgtggtaa ccactgttcc gaagccttcc tcagtacaat ctgtggctgt gccaacctgt 420
34 rgctgcacac gttactcctg gaaagccatt gaatactgta actaccctga agccttcaag 480
35 tttgggagca tcatccactc cttcaaatga gcccaatctt aaagcagaga actcagcagc 540
36 tgttcagatt aatctttctc cgacaatgct agaaaatgtg aagaaatgca agaacttctt 600
37 tgcaatgtta ataaaactag catgtagtgg atcacagtcc cctgaaatgg ggcaaatgt 660
38 gaagaagctg gtggaacaac ttttggtatgc aaaaatcgaa gcagaagaat ttactaggaa 720
39 actgtatggt gaactcaagt cttcacctca gccctacctg gttccttttc ttaagaaaag 780
40 cgtgggtgcc ttacgacaa tctgcctaa cctccagagc ttcattccagc aatgtgttca 840
41 gcagacttct agtgacatgg tcattgctac ctgtactaca acagtaacaa cttctcctgt 900
42 ggtgacaact acagtgtcct caagccagtc tgaaaagtca attattgttt ctggagcaac 960
43 agcaccacga actgtgtcag tgcaaaacttt gaaccactt gctggtccag tgggagcaaa 1020
44 agctggagtt gtgacacttc attctgtggg cccaactgct gcaacaggag gaacaacagc 1080
45 tggaaactgg ttgcttcaga cttcaaaacc acttgtgaca tctgtggcaa acacagtgc 1140
46 caggtgttca ctgcaacctg aaaagccagt tgtctctgga acagcagtaa cactgtcctt 1200
47 tccagcagta acttttgagg aaacttcagg tgcagctatt tgtcttccat ctgtgaaacc 1260
48 tgttggttcc ttctgctggg accacatctg caagcctgtt attgggactc cagttcaaatt 1320
49 caaacttgcc cagccggggc ctgtcctttc acaaccagct gggattccaa caggcagttc 1380
50 aagcaagcaa ctattctcat tgtttcacgt agttcagcag ccttcaggag gcaatgaaaa 1440
51 acaagtgaac acaatttcac attcctcaac attgaccatt cagaaatgtg gacagaagac 1500
52 gatgccagtg aacaccataa tacctactag tcagtttctt ccagcttcca ttctaaagca 1560
53 aattacctct gcctggaaat aaaattctgt cacttcaagc atctcctact cagaaaaata 1620
54 gaataaaaaga gaatgtaaca tcatgcttcc gagatgagga tgacatcaat gatgtgactt 1680
55 ctatggcagg ggtcaacctt aatgaagaaa atgacctgat cttagcaaca aactctgaat 1740
56 tggttggcac actcattcag tcatgtaaa atgaaccatt tctttttatt ggagctctac 1800
57 aaaagagaat cttagacatt ggtaaaaagc atgacattac agaacttaac tctgatgtc 1860
58 tgaacttgat ctcccaagca acacaggaac gactacgagg ccttctagaa aaactgactg 1920

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59 caattgctca gcatcgaatg actacttaca aggcaagtga aaattacatc ctgtgtagtg 1980
60 ataccaggtc acagctcaaa tttcttgaaa agctggatca attggagaag cagagaaagg 2040
61 atttgaaga aagagaaatg ttacttaagg cagccaagag tcgttctaataaagaagatc 2100
62 cagaacagct gagattaaag cagaaagcca aagagttaca gcaattggaa cttgcacaga 2160
63 tacagcatag agacgctaata ctcacagctc ttgcagctat tggaccaagg aagaagagac 2220
64 cactagaatc tgggaattgag ggcttaaaag acaaccttct tgcttctggg acatccagcc 2280
65 tgacagccac caaacagttg catcgcccaa gaatcacgag aatctgcctc agggacttga 2340
66 tattttgtat ggaacaggaa cgggagatga agtattctcg agctctatac ctggcccttc 2400
67 tgaagtgacc actccactct tccatccaca tcttgctat ttactgcaa agaagacaca 2460
68 aagcattgtt gcaactgtcct gaaatttcaa tttctggaaa ataacaccaa catgaaagag 2520
69 cattgtttac gattagaact ttattaactc ttacctat 2558
71 <210> SEQ ID NO: 2
72 <211> LENGTH: 852
73 <212> TYPE: PRT
74 <213> ORGANISM: Homo sapiens
76 <400> SEQUENCE: 2
77 Gly Thr Leu Val Thr Lys Val Ala Pro Val Ser Ala Pro Pro Lys Val
78 1 5 10 15
79 Ser Ser Gly Pro Arg Leu Pro Ala Pro Gln Ile Val Ala Val Lys Ala
80 20 25 30
81 Pro Asn Thr Thr Thr Ile Gln Phe Pro Ala Asn Leu Gln Leu Pro Pro
82 35 40 45
83 Gly Thr Val Leu Ile Lys Ser Asn Ser Gly Pro Leu Met Leu Val Ser
84 50 55 60
85 Pro Gln Gln Thr Val Thr Arg Ala Glu Thr Thr Ser Asn Ile Thr Ser
86 65 70 75 80
87 Arg Pro Ala Val Pro Ala Asn Pro Gln Thr Val Lys Ile Cys Thr Val
88 85 90 95
89 Pro Asn Ser Ser Ser Gln Leu Ile Lys Lys Val Ala Val Thr Pro Val
90 100 105 110
91 Lys Lys Leu Ala Gln Ile Gly Thr Thr Val Val Thr Thr Val Pro Lys
92 115 120 125
93 Pro Ser Ser Val Gln Ser Val Ala Val Pro Thr Ser Val Val Thr Val
94 130 135 140
95 Thr Pro Gly Lys Pro Leu Asn Thr Val Thr Thr Leu Lys Pro Ser Ser
96 145 150 155 160
97 Leu Gly Ala Ser Ser Thr Pro Ser Asn Glu Pro Asn Leu Lys Ala Glu
98 165 170 175
99 Asn Ser Ala Ala Val Gln Ile Asn Leu Ser Pro Thr Met Leu Glu Asn
100 180 185 190
101 Val Lys Lys Cys Lys Asn Phe Leu Ala Met Leu Ile Lys Leu Ala Cys
102 195 200 205
103 Ser Gly Ser Gln Ser Pro Glu Met Gly Gln Asn Val Lys Lys Leu Val
104 210 215 220
105 Glu Gln Leu Leu Asp Ala Lys Ile Glu Ala Glu Glu Phe Thr Arg Lys
106 225 230 235 240
107 Leu Tyr Val Glu Leu Lys Ser Ser Pro Gln Pro His Leu Val Pro Phe
108 245 250 255
109 Leu Lys Lys Ser Val Val Ala Leu Arg Gln Leu Leu Pro Asn Ser Gln

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110      260      265      270
111 Ser Phe Ile Gln Gln Cys Val Gln Gln Thr Ser Ser Asp Met Val Ile
112      275      280      285
113 Ala Thr Cys Thr Thr Thr Val Thr Thr Ser Pro Val Val Thr Thr Thr
114      290      295      300
115 Val Ser Ser Ser Gln Ser Glu Lys Ser Ile Ile Val Ser Gly Ala Thr
116 305      310      315      320
117 Ala Pro Arg Thr Val Ser Val Gln Thr Leu Asn Pro Leu Ala Gly Pro
118      325      330      335
119 Val Gly Ala Lys Ala Gly Val Val Thr Leu His Ser Val Gly Pro Thr
120      340      345      350
121 Ala Ala Thr Gly Gly Thr Thr Ala Gly Thr Gly Leu Leu Gln Thr Ser
122      355      360      365
123 Lys Pro Leu Val Thr Ser Val Ala Asn Thr Val Thr Thr Val Ser Leu
124      370      375      380
125 Gln Pro Glu Lys Pro Val Ser Gly Thr Ala Val Thr Leu Ser Leu
126 385      390      395      400
127 Pro Ala Val Thr Phe Gly Glu Thr Ser Gly Ala Ala Ile Cys Leu Pro
128      405      410      415
129 Ser Val Lys Pro Val Val Ser Phe Cys Trp Asp His Ile Cys Lys Pro
130      420      425      430
131 Val Ile Gly Thr Pro Val Gln Ile Lys Leu Ala Gln Pro Gly Pro Val
132      435      440      445
133 Leu Ser Gln Pro Ala Gly Ile Pro Thr Gly Ser Ser Ser Lys Gln Leu
134      450      455      460
135 Phe Ser Leu Phe His Val Val Gln Gln Pro Ser Gly Gly Asn Glu Lys
136 465      470      475      480
137 Gln Val Thr Thr Ile Ser His Ser Ser Thr Leu Thr Ile Gln Lys Cys
138      485      490      495
139 Gly Gln Lys Thr Met Pro Val Asn Thr Ile Ile Pro Thr Ser Gln Phe
140      500      505      510
141 Pro Pro Ala Ser Ile Leu Lys Gln Ile Thr Leu Pro Gly Asn Lys Ile
142      515      520      525
143 Leu Ser Leu Gln Ala Ser Pro Thr Gln Lys Asn Arg Ile Lys Glu Asn
144      530      535      540
145 Val Thr Ser Cys Phe Arg Asp Glu Asp Asp Ile Asn Asp Val Thr Ser
146 545      550      555      560
147 Met Ala Gly Val Asn Leu Asn Glu Glu Asn Ala Cys Ile Leu Ala Thr
148      565      570      575
149 Asn Ser Glu Leu Val Gly Thr Leu Ile Gln Ser Cys Lys Asp Glu Pro
150      580      585      590
151 Phe Leu Phe Ile Gly Ala Leu Gln Lys Arg Ile Leu Asp Ile Gly Lys
152      595      600      605
153 Lys His Asp Ile Thr Glu Leu Asn Ser Asp Ala Val Asn Leu Ile Ser
154      610      615      620
155 Gln Ala Thr Gln Glu Arg Leu Arg Gly Leu Leu Glu Lys Leu Thr Ala
156 625      630      635      640
157 Ile Ala Gln His Arg Met Thr Thr Tyr Lys Ala Ser Glu Asn Tyr Ile
158      645      650      655

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```

159 Leu Cys Ser Asp Thr Arg Ser Gln Leu Lys Phe Leu Glu Lys Leu Asp
160           660           665           670
161 Gln Leu Glu Lys Gln Arg Lys Asp Leu Glu Glu Arg Glu Met Leu Leu
162           675           680           685
163 Lys Ala Ala Lys Ser Arg Ser Asn Lys Glu Asp Pro Glu Gln Leu Arg
164           690           695           700
165 Leu Lys Gln Lys Ala Lys Glu Leu Gln Gln Leu Glu Leu Ala Gln Ile
166 705           710           715           720
167 Gln His Arg Asp Ala Asn Leu Thr Ala Thr Ala Ala Ile Gly Pro Arg
168           725           730           735
169 Lys Lys Arg Pro Leu Glu Ser Gly Ile Glu Gly Leu Lys Asp Asn Leu
170           740           745           750
171 Leu Ala Ser Gly Thr Ser Ser Leu Thr Ala Thr Lys Gln Leu His Arg
172           755           760           765
173 Pro Arg Ile Thr Arg Ile Cys Leu Arg Asp Leu Ile Phe Cys Met Glu
174 770           775           780
175 Gln Glu Arg Glu Met Lys Tyr Ser Arg Ala Leu Tyr Leu Ala Leu Leu
176 785           790           795           800
177 Lys Glx Pro Leu His Ser Ser Ile His Ile Leu Ala Ile Tyr Cys Gln
178           805           810           815
179 Arg Arg His Lys Ala Leu Leu His Cys Pro Glu Ile Ser Ile Ser Gly
180           820           825           830
181 Lys Glx His Gln His Glu Arg Ala Leu Phe Thr Ile Arg Thr Leu Leu
182           835           840           845
183 Thr Leu Thr Tyr
184           850

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186 <210> SEQ ID NO: 3

187 <211> LENGTH: 30

188 <212> TYPE: DNA

189 <213> ORGANISM: Artificial Sequence

191 <220> FEATURE:

192 <223> OTHER INFORMATION: NFkB Oligonucleotide

194 <400> SEQUENCE: 3

195 agcttaggga ctttccgagg ggactttccg

30

197 <210> SEQ ID NO: 4

198 <211> LENGTH: 30

199 <212> TYPE: DNA

200 <213> ORGANISM: Artificial Sequence

202 <220> FEATURE:

203 <223> OTHER INFORMATION: NFkB Oligonucleotide

205 <400> SEQUENCE: 4

206 gatccggaaa gtcccctcgg aaagtccta

30

208 <210> SEQ ID NO: 5

209 <211> LENGTH: 30

210 <212> TYPE: DNA

211 <213> ORGANISM: Artificial Sequence

213 <220> FEATURE:

214 <223> OTHER INFORMATION: Mutated NFkB Oligonucleotide

216 <400> SEQUENCE: 5

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217 agcttatcta ctttccgagt ctactttccg      30
219 <210> SEQ ID NO: 6
220 <211> LENGTH: 30
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Mutated NFkB Oligonucleotide
227 <400> SEQUENCE: 6
228 gatccggaaa gtagactcgg aaagtagata      30
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VERIFICATION SUMMARY

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Input Set : A:\13005 002001.TXT

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